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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Direct Submission
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Pred. No. 7.4e-205;
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                 Submitted (04-FEB-2000) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, Genome Center
                                                                            Direct Submission
Submitted (03-FEB-2000)
University, 4444 Forest
4 (bases 1 to 132953)
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Submitted (20-OCT-1997)
University, 4444 Forest
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Human BAC clone GS1-113H23 :
AC003015
AC003015.1 GI:2547255
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                                                                                                                                                   Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108,
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------Summary Statistics
Center project name: H_GS113H23
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by confirmed sequence from more than one subclone; and the assembly was ${\bf i}$ by restriction digest.

MAPPING INFORMATION:

Medicine, St. Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University School Louis MO. of.

Mapping information for this clone was also provided by Dr. Michael Lovett, Departments of Otorhinolaryngology, Molecular Biology and Oncology, University of Texas Southwestern Medical Center, Dallas

SOURCE INFORMATION:

(http://www.genomesystems.cell line: lymphoblastoid Haplotypes: two VECTOR: pBeloBAC This clone is from the first . com). BAC library from Genome Systems,

Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is GS1-330J10,
Actual start of this clone is at base position
actual end is at 132953 of GS1-113H23. , 200 1 of 00 bp overlap. of GS1-113H23;

This clone contains STS HSC022YA5 (NID:9454585). (NID:g1235481) and

This clone contains polymorphisms
Location/Qualifiers with

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/clone_lib="GSBAC1"
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family-"MER"

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899; Conserva
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1. 146296
                                                                                                                                                                                                                                                                                                      Submitted (15-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Aug 15, 2001 this sequence version replaced gi:13173629. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-MAR 2001) DOE Joint Genome Insti
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 146296)
DOE Joint Genome Institute and Stanford Human
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                                                                                                                                                                                                                                                                                   Finishing Completed at Stanford Human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146296)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Joint Genome Institute.
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Eukaryota; Eutheria; Primates; Ca
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 14774)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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HTG; HTGS_PHASE2; HTGS_DRAFT
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Consensus quality: 137633 bases at least Q30
Consensus quality: 139230 bases at least Q20
Estimated insert size: 128750; agarcse-fp estimation
Estimated insert size: 128750; sum-of-contigs estimation
Quality coverage: 5.08 in Q20 bases; agarcse-fp estimation
Quality coverage: 4.64 in Q20 bases; sum-of-contigs estimation
**NOTE: This is a "working draft" sequence. It currently
**consists of 16 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * by the finished sequence as soon as it is available and the accession number will be preserved.

* the accession number will be preserved.

* 21583 21582 contig of 21582 bp in length

* 21583 21682: gap of unknown length length

* 34006 34105: contig of 12233 bp in length

* 34106 37105: contig of 3000 bp in length

* 37106 37105: gap of unknown length

* 37106 37205: gap of unknown length

* 37206 39674: contig of 2469 bp in length

* 39675 39774: gap of unknown length

* 39675 39774: gap of unknown length
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Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gl:7712070.
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                                                                                                                                            Location,
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141747: contig
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14: contig of 2341
14: gap of unknown
B7: contig of 7673
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Direct Submission
Submitted (21-JAN-2000) NIDCR, NIH, Drive, Bethesda, MD 20892, USA
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Adler, E., Hoon, M.A.,
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/protein_id="AAF43913.1"
/db_xref="GI:7262627"
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Sequence 78
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T2r taste receptor family
Patent: WO 0118050-A 78 15-MAR-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
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Mammalia; Eutheria;
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/note="rat T2R01, rGR01"
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And Zuker, C.S.

Direct Submission

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HALVSAMLSILSFLIILLSHDMVAVLICTQGLHFGSRTFAFCLLVIGMYPSLHSIVLI
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/db_xref="GI:7262645"
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/strain="129/SvJ"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musinae; 
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1 (bases 1 to 957)

Zuker, C. S., Adler, J. E., Ryba, N., Mueller, K. and Hoon, M.

Tar taste receptor family

Patent: WO 0118050-A 14 15-MAR-2001;

THE RECENTS OF THE UNIVERSITY OF CALIFORNIA (US); THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

LOCALION/Qualifiers
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/db_xref="taxon:9606"
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Adler,E., Hoon,M.A., I
and Zuker,C.S.
Direct Submission
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                                                                                                           Adler,E., Hoon,M.A., Mueller,K.L., zuker,C.S.
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Location/Qualifiers
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YPSSHSFILILGNNKLRHASLKVIWKVMSILKGRKFQQHKQI"
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DLILTSLAISRICLLCYILLDCFILVLYPDYYATGKEMRIIDFFWTLTNHLSIWFATC
LSIYYFFKIGNFFHPLFLMMKWRIDRYISWILLGCYVLSYFISLPATENLNADFRECY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="G protein-coupled receptor; PCR-derived similar to an interval in BAC AC006518"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="candidate taste receptor T2R7"
/protein_id="AAF43906.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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               CIONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                         submitted (01-MAY-1999) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Apr 29, 1999 this sequence version replaced gi:4589934.
INFORMATION: http://www.hgsc:bcm.tmc.edu/ or email
Overlapping clones are noted at the beginning \mbox{\sc Features} listing.
                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H., Gorrell,L.L., Hernandez,J., 'Issar,A., Jackson,L., Kneitz,S., Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W., Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A., Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L., Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M., Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W., Zhou,X., Kucherlapati,R., Nelson,D. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 173735)
                                                                                                                                                                                    gc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Homo sapiens 12p13 BAC RPCII1-144023
Human BAC Library) complete sequence.
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BAC RPCII1-144023 (Roswell Park Cancer Ins
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                                                                                                                                                                                                                                                                                                 Department
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STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

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OWALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT----

bases	Position 31176 31177 104155	Contig length; Phrap values i Average error Fraction of Ph Number of Cons Number of N's
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* * *	Consensus changing ed: Original+Context 9t9999t999(n)agag9999ag t9999t999(n)agag999ag gagtttcact(n)tgttgtcctc Distribution of Quality < 40	wp ct
****	lts Ba	estimate): than 40: adits:
******	Edited+Context gtgggttggg(g)gagggggag gagtttcact(c)tgttgtcctc	173735 167393 0.000263256 0.0395058 3

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1873. 1957 1.01Location/Qualifiers
1. .173735 /rpt_family="MER53" otxp

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10

Phrap Value 15

35

60

ANNOTATION OF FEATURES

Indels

Gaps

<u>ن</u>

60

1362

Length 173735; 24;

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complement(13954. .1
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1301 GTAATACTATTAGATTGTTTTATATTGGTGCTATATCCAGATGTCTATGCCACTGGTAAA 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1361 ATTGCCTCCATTGATTTAATCCTCACAAGTCTGGCCATATCCAGAATTTGTCTATTGTGC 1302
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                                                                                                          641 CATTCATTTATCCTAATACTGGGGAACAATAAATTAAGACATGCATCTCTAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 attttcacaaatggcatcattgtggtggtggaatggcattgacttgatcaagcacagaaaa 120
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      AC068649 190002 bp
Homo sapiens chromosome
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complement(32384. .33480)
/rpt_family="LIMA5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 124.4; DB 9;
Pred. No. 2.7e-19;
0; Mismatches 421;
      DNA HTG 17-JUL-2001
12 clone RP11-377C14, WORKING DRAFT
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1002

466

519

942

579

1122

288

408

repeat_region repeat_region

repeat_region repeat_region

> 816 702

759

642

699 822 639

repeat_region repeat_region

VERSION KEYWORDS SOURCE

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JOURNAL
REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 17, 2001 this sequence version replaced gi:14547698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tangy, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Washington, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davia, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davia, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Davis, C., Chen, R., Ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                              Center project Information
Center project name: HMDR
Center clone name: HMDR
Center clone name: Plans
Sequencing vector: Plasmid; M77789
Sequencing vector: M13; LO8821
Chemistry: Dye-primer Bodipy: 24% of reads
Chemistry: Dye-terminator Big Dye: 76% of rea
Assembly program: Phrap; version 0.990329
Consensus quality: 191018 bases at least 040
Consensus quality: 191018 bases at least 030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 190002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
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                                        least Q40
least Q30
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580 gttttgctcttgattttctctctggggaggcacacccggcaaatgagaaacacagtggcc 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
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COMMENT

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Db 137346 TCTGTGTTTATTAGCCTTCCAGCCACTGAGAATTTGAACGCTGATTTCAGGTTTTGTGTG 137405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 137046 ATTGCCTCCATTGATTTAATCCTCACAAGTCTGGCCATATCCAGAATTTGTCTATTGTGC 137105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 136986 ATCTTAGGGAATGCATTCATTGGATTGGTAAACTGCATGGACTGGGTCAAGAAGAAGGAAA 137045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 136926 ATGGCAGATAAAGTGCAGACTACTTTATTGTTCTTAGCAGTTGGAGAGTTTTCAGTGGGG 136985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
467 taaggaaatttttctcccaaaatgcca-----caattcaaaaagaagatacactggct 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ttcatcttctacgttaatgtgattgttatcttcttcatagaatt-----catcatgt 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atgctagagtctcacctcattatctattttcttcttgcagtgatacaatttcttcttggg 60
                                                atacagattttctctttttgttgctgagttctcagtgccattgcttatcttccttttttgct 579
                                                                                                   gttctgcgaattgtgcaattctctt----atttataaatgaattggaactttggcttgcc 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAATACTATTAGATTGTTTTATATTGGTGCTATATCCAGATGTCTATGCCACTGGTAAA 137165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atggctccgctggatctcctttctttgtctggcagtttctagaatttttcttgcagttg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attttcacaaatggcatcattgtggtggtgaatggcattgacttgatcaagcacagaaaa 120
                                                                                                                                                                                                                                                                                                                                         tggttgaagatgaggatatccaagctggtcccatggatgatcctggggtctctgctatat 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATGAGAATCATTGACTTCTTCTGGACACTAACCAATCATTTAAGTATCTGGTTTGCA 137225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence {\bf r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158237
158337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP11-377C14"
34404 c 34985 g
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .190002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158236: contig of 158236 bp in length 158336: gap of unknown length 190002: contig of 31666 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qualifiers
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                                                             GTCTGGACATTTGCCAATAATTCAAGTCTCTGGTTTACTTCTTGCCTCAGTATCTTCTAT
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1 (bases 1 to 939)
Zuker, C.S., Adler, J.E., Ryba, N., Mueller, K.
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/db_xref="taxon:9606"
/note="human T2R09, hGR09"
187 c 186 g 318
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Pred. No. 3.7e-19;
0; Mismatches 418;
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                                                                                                                                                         Adler,E., Hoon,M.A., Mueller,K.L.,
and Züker,C.S.
Direct Submission
Submitted (21-JAN-2000) NIDCR, NIH,
Drive, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                          Zuker,C.S.
A novel family of mammalian taste Cell 100 (6), 693-702 (2000)
20222571
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AF227135
AF227135.1 GI:7262616
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            /note="G protein-coupled receptor; PCR-derived sequence;
similar to an interval in BAC AC006518"
/codon_start=1
                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/map="12p13"
/product="candidate taste
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                                                                                                                                                                                                        CACACCAAGCAGATTCGACTGCATGCTACAGGGTTCAGAGACCCCCAGTACAGAGGCCCCAC
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/translation="MP6AIEAIVIILIAGELTIGIWGNGFIVLVNCIDWLKRRDISLI
DIILISLAISRICULCVISLOGFEMLLFPGTYGNSVLVSIVNVVWTFANNSSLWETSC
LSIFYLLKIANISHPFFFWLKLKINKVWLAILLGSFLLSLIISVPKNDDMWYHLFKYS
HEENITWKFKVSKIPCTFKQLTLNLGVWVPFTLCLISFFLLLFSLVRHTKQIRLHATG
FRDPSTEAHWRAIKAVIIFLLLLIVYYPVFLVMTSSALIPQGKLVLMIGDIVTVIFPS
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0; Mismatches 418;
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Search completed: December 11, 2001, 02:40:45 Job time: 8462 sec

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Page 16

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Human GTP-binding
Human T2R03 nucleo
Mouse T2R30 nucleo
Human T2R30 nucleo
Polynucleotide seq
                                                                                                                                 Human T2R01 nucleo
Rat T2R01 nucleoti
Mouse T2R19 nucleo
Human T2R07 nucleo
Human T2R09 nucleo
Human T2R33 nucleo
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Oligonucleotide Dl	82	22	ū	9.0	0	45
Oligonucleotide Dl	582	22	Ü	•	0	44
Oligonucleotide D1	82	22	ū	•	80.6	43
Mouse T2R01 nucleo	925	22	7	•	<u>ب</u>	42
Mouse T2R02 nucleo	925	22	U	•	N	.41
Mouse T2R13 nucleo	25	22	9	٠	83	40
1 T2R02	25	22	$\overline{}$	•	Ψ	39
onucleo1	582	22	w	9.4	84.4	38
gonucleotide	82	22	w	•	٠.	37
nucleotide	82	22	w	•		36
	82	22	w	•	4.	35
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e T2R15	LJI	22	8		9	28
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T2R08	25	22	u	•	.7	26
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secre	AAD05535	22	1122	9.8	88.6	23
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T2R31	25	22	0	0	0.6	20 ~
an T2R05 nucle	25	22	0	9	:	19
2R0	25	22	5	0		18
an T2	25	22	-	•		17
T2R0	25	22	30	۲.		16
e T2	25	22	ш	۲	<u>. </u>	15
e T2	925	22	56	•	ω.	14 .
T2R25 nucle	925	22	10	•		13
Human T2R15 nucleo	AAF92515	22	0		7.	12

ALIGNMENTS

RESULT AAF92502

16-MAY-2001 (first entry)

AAF92502;

AAF92502 standard;

DNA; 900

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DE Human T2R01 nucleotide sequence SEQ ID NO:2.

XX

KW

Human; rat; mouse; T2R; taste receptor; G-protein coupled receptor; KW

KW

KW

taste transduction G-protein coupled receptor; identification; tongue;
KW

taste sensory neuron; taste cell; taste modulator; food;
XX

COS

Homo sapiens.

XX

PN

W0200118050-A2.

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PD

15-MAR-2001.

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PF

08-SEP-2000; 2000WO-US24821.

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PR

10-SEP-1999; 99US-0393634.

PR

22-FEB-2000; 2000US-0510332.

XX

PA

(REGC) UNIV CALIFORNIA.

PA

(USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PA

ZUKER CS, Adler JE, Ryba N, Mueller K, Hoon M;
XX

WP: 2001-211396/21.

DR

P-PSDB; AAB87731.
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Query Match
Best Local Similarity
Matches 900; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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           transduction G-protein coupled receptors designated T2R proteins.

CC AABB7731 to AABB7824 represent T2R proteins, and AABB7825 to AABB7830

CC represent T2R family consensus sequences from the present invention.

CC The T2R proteins are taste modulators. The nucleic acids are useful as cc probes for the identification of taste cells, as the nucleic acids are cspecifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship to taste centres in the brain. The taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for the transcription of taste signalling pathways.

CM Modulatory compounds comprising T2R proteins can therefore be used in the food and pharmaceutical industries to customise taste, for e.g. to
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                                                                                                                                                                                                                                                                                                                                                          AAF92502 to AAF92572 represent nucleic acids which encode taste

C transduction G-protein coupled receptors designated T2R proteins.

AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830

C represent T2R family consensus sequences from the present invention.

The T2R proteins are taste modulators. The nucleic acids are useful as

probes for the identification of taste cells, as the nucleic acids are

specifically expressed in taste cells. They also serve as tools for the

generation of taste topographic maps that elucidate the relationship

between the taste cells of the tongue and taste sensory neurons leading

to taste centres in the brain. The taste modulators are useful for

pharmacological and genetic modulation of taste signalling pathways.

Modulatory compounds comprising T2R proteins can therefore be used in

food and pharmaceutical industries to customise taste, for e.g. to

c decrease the bitter taste of food or drugs.
                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be us food and pharmaceutical industries to customize taste, for e.g. t decrease the bitter taste of food .
                                                                                                                                                                                                                                                                                                                                      Sequence 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 51; Page 231; 249pp; English.
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P-PSDB; AAB87813.
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(USSH ) US DEPT HEALTH & HUMAN
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tgtatattgtttgcacagctgggtctatcctgtttggtgagacacacgttatttgctgac
                            ttoatottotacgttaatgtgattgttatcttcttcatagaattcatcatgtgttctgcg 240
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                                                                                                                                                                                                                                                                         Similarity
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22-FEB-2000;
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Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be used food and pharmaceutical industries to customize taste, for e.g. to decrease the bitter taste of food -
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Disclosure;

Page 165-166; 249pp; English.

probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for pharmacological and genetic modulation of taste signalling pathways. Modulatory compounds comprising T2R proteins can therefore be used in food and pharmaceutical industries to customise taste, for e.g. to decrease the bitter taste of food or drugs. AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AAB87731 to AAB87824 represent T2R proteins, and AAB8755 to AAB87830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as

Sequence 957 BP; 256 A; 202 C; 192 G; 307 T; 0 other;

Query Match Best Local S Matches 451

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Score 124.4; DB 22; Pred. No. 2.5e-24; 0; Mismatches 421;

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                                                                                                                                                                                                                                                                           AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC )
                                                                                                                                                                                                                        pharmacological and genetic modulation of taste signalling pathways. Modulatory compounds comprising T2R proteins can therefore be used i food and pharmacoutical industries to customise taste, for e.g. to decrease the bitter taste of food or drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 182-183; 249pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be us food and pharmaceutical industries to customize taste, for e.g. t decrease the bitter taste of food -
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31-MAR-2000;
23-MAY-2000;
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AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AAB87831 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading
                                                                                                                                                                       Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be us food and pharmaceutical industries to customize taste, for e.g. t decrease the bitter taste of food -
                                                                                                                                                Disclosure; Page 162; 249pp;
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                                                                                                                                                                                                                                          AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste topographic maps that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for pharmacological and generic modulation of taste signalling pathways. Modulatory compounds comprising T2R proteins can therefore be used in food and pharmacoutical industries to customise taste, for e.g. to decrease the bitter taste of food or drugs.
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taste transduction G-protein coupled receptor; identification; tongue;
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C AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830
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Modulatory compounds comprising T2R proteins can therefore be used in food and pharmaceutical industries to customise taste, for e.g. to decrease the bitter taste of food or drugs.
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Pred. No. 5.4e-20;
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signal sequence cloning; hybridization cloning; gene therapy;
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Query Match Best Local

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DB 20;

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The PNs and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hemostatic activity, chemotactic/chemokinetic activity, hemostatic activity.
                                                                              and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumor invasion suppressor activity, and tumor inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as e.g. weight, color, skin, etc. effecting biorhythms or circadian cycles; enhancing fertility; treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the polynucleotide sequence of the clone pt127_1, which was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins, or by identification as a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding human secreted proteins used therapeutic, diagnostic and research purposes.
                                                         depression; treatment of pain; hormonal or endocrine activity.
2695 BP; 858 A; 427 C; 486 G; 919 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnostic and research purposes
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                       transduction G-protein coupled AAB87731 to AAB87824 represent represent T2R family consensus
                                                                                                                                                                                                Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be us food and pharmaceutical industries to customize taste, for e.g. t decrease the bitter taste of food -
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22-FEB-2000;
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                                                                                              AAF92502 to AAF92572 represent nucleic acids which encode taste
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                                                                                                                                                 AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AABB731 to AABB7824 represent T2R proteins, and AABB7825 to AABB7830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are specifically expressed in taste cells. They also serve as tools for the generation of taste cells that elucidate the relationship between the taste cells of the tongue and taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for pharmacological and genetic modulation of taste signalling pathways. Modulatory compounds comprising T2R proteins can therefore be used in
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                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be used food and pharmaccutical industries to customize taste, for e.g. to decrease the bitter taste of food -
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taste transduction G-protein coupled receptor; identification; tong
10-SEP-1999;
22-FEB-2000;
                                       08-SEP-2000; 2000WO-US24821.
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2000US-0510332
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Ct transduction G-protein coupled receptors designated T2R proteins.

CC AABB7731 to AABB7824 represent T2R proteins, and AABB7825 to AABB7830

CC represent T2R family consensus sequences from the present invention.

CC The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are generation of taste topics, as the nucleic acids are compounds to the tongue and taste serve as tools for the compounds compounds compounds to taste sensory neurons leading to taste centres in the brain. The taste modulators are useful for pharmacological and generic modulation of taste signalling pathways.

CC Modulatory compounds comprising T2R proteins can therefore be used in food and pharmaceutical industries to customise taste, for e.g. to very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local (
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                                      489
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AAF92502 to AAF92572 represent nucleic acids which encode taste transduction G-protein coupled receptors designated T2R proteins. AAB87731 to AAB87824 represent T2R proteins, and AAB87825 to AAB87830 represent T2R family consensus sequences from the present invention. The T2R proteins are taste modulators. The nucleic acids are useful as probes for the identification of taste cells, as the nucleic acids are
                                                                                                                         Nucleic acids encoding the T2R family of G-protein coupled taste receptors, useful for identifying taste modulators that can be us food and pharmaceutical industries to customize taste, for e.g. t decrease the bitter taste of food .
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Search completed: December 11, 2001, 02:39:56

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Nat. Biotechnol. 19 (5), 440 (2
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, 0
Tel: 216 431 9900
Fax: 216 361 9596 BG209561 RST29087 BG209561 Email: scain@athersys.com
High quality sequence stop: 557.
Location/Qualifiers and Ducar,M.

Creation of Genome-wide Protein Expression Libraries using Random Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 806) Homo sapiens BG209561.1 GI:13731248 /organism="Homo sapiens"
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/clone_lib="Athersys RAGE Library"
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Libraries using Random Activation of Gene Expression', Athersys 908 RAGE Library Homo sapiens cDNA, mRNA (2001) In press OH 44115, mRNA sequence. 21-APR-2001

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Contact: Shaying Zhao, William Nierma
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are availabe from Research Gen
                                                                                                                                                                                                                                                                                                                     CTGCTATATGTATCTATGATTTGTGTTTTTCCATAGCAAATATGCAGGGTTTATGGTCCCA
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/clone 142 --
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/note="vector: pBeloBAC11;
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Email: hbe@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mi3-21
Class: BAC ends. '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shaying Zhao, William Niern
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 650)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K. Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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/db_xref="taxon:9606"
/clone="2530B7"
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EST.
                                                        3201 Carnegie Ave,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                          Activation of Gene Expression Nat. Biotechnol. 19 (5), 440 Contact: Scott J. Cain
                                                                                                                                      Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 758)
                                                                                                                      Creation of Genome-wide Protein
                                                                                    Athersys, Inc.
                                                                                                                                     and
                                                                                                                                                                                                                          human.
                                                                                                                                     Ducar, M
                                     l: scain@athersys.com
quality sequence stop
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Athersys
                         ity sequence stop: .
Location/Qualifiers
/organism≃"Homo sapiens"
/db_xref="taxon:9606"
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RAGE Library Homo sapiens
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  sequence.
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Berry,K., Granger,D.,
Venter,J.C.
                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/cell_line-"HT1080"
/note-"See 'Creation of Genome-wide Protein Expression
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95.8%;
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Pred. No. 7.3e-101;
0; Mismatches 23;
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                                             Craniata; Vertebrata; Catarrhini; Hominidae.
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
Other_GSSs: CITBI-E1-2516A7
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 261) Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end search page:
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                                                                 Homo sapiens
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Athersys RAGE Library
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/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2:
CalTech Human BAC Library D"
CalTech Human BAC Library D"
1 77 c 69 g 88 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2516A7"
/clone_lib="CITBI-El"
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Pred. No. 3.5e-53;
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 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
                                                                                                                                                                                                                  AA416581 463 bp mRNA EST 16-OCT-1997 zu05e04.sl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730974 AA416581
                                                                                                                                                                                    AA416581.1 GI:2077515
EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 216 361 9596
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3201 Carnegie Ave, Cleveland, OH
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Veloso,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.
                                                                                             (bases 1 to 463)
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/Cell_line="MT1080"
/note="See 'Creation of Genome-wide Protein Expression
/Libraries using Random Activation of Gene Expression',
Rature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/db_xref="taxon:9606"
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Pred. No. 8.8
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                                                                                                                                                                                                                                                                                                                                                                      251;
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BG188332.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; F
1 (bases 1 to 321)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whitti
Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,F
                                                                               Homo sapiens
                                                                                                                                        BG188332 321 bp mRNA EST 21-APR-2001 RST7350 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
Washington University School of Medicine
                                                                                             human
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Tel: 314 286 1800
Fax: 314 286 1810
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/clone="IMAGE:730974"
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/db_xref="GDB:5927764"
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             Whittington, J
                                                              Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Activation of Gene Express Nat. Biotechnol. 19 (5), 4 Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J
and Ducar, M.
Creation of Genome-wide Protein Expression Libraries
Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, Research Center (DKFZ); Email s.wiemann@dkfz- heis sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Athersys, Inc.
3201 Carnegie Ave,
                                                                                                                                                                                                                                                                                      AL037695 554 bp mRNA EST DKFZp56400672_r1 564 (synonym: hfbr2) Homo DKFZp56400672 5', mRNA sequence.
                                                                                                        Unpublished (1999)
On Jul 7, 1999 this
                                                                                           Contact: Blum H
                                                                                                                                        EST (Blum,
                                                                                                                                                      Blum, H., Bauersachs, S.,
                                                                                                                                                                      Mammalia; Eutheria;
1 (bases 1 to 554)
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216 361 9596
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/clone_lib="Nthersys RAGE Library"
/clone_lib="Nthersys RAGE Library"
/cell_line="HT1080"
/notc="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Blotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ity sequence stop: .
Location/Qualifiers
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                                                                                                                                        et al.)
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98.3%;
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Primates;
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Pred. No. 3.8e-38;
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                 heidelberg.de;
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VERSION KEYWORDS SOURCE

ORGANISM

human

Homo sapiens Eukaryota; Me Mammalia; Eut

; Metazoa; Eutheria;

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

ACCESSION DEFINITION

AQ103952 383 bp DNA GSS HS_3107_A1_C05_T7 CIT Approved Human Genomic sapiens genomic clone Plate=3107 Col=9 Row=E, AQ103952 GSS.

Sperm Library

Homo

AQ103952 LOCUS

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$1 sequence also available.

$1 sequence (DK72p56400672) is available at the This clone (DK72p56400672). Ressourcezentrum, Heep Please contact the RZPD: RZPD: RZPD: RZPD: RZPD: RZPD: RZPD: RZPD: RZPD: RZPD
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/clone="DKF2p56400672"
/clone_lib="564 (synonym: h
/tissue_type="brain"
/dev_stage="fetal"
/lab_bost="X1-2blue"
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96 c 108 g
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48.9%;
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Pred. No. 2.2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 253;
   515
                                                           524
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196 t
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les 108; Conserv
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                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 589)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Adams, M.D., a
                                                                                                                                                                                                                                   AQ590563 589 bp DNA
HS_5400_A1_G04_T7A RPCI-11 Human Male
genomic clone Plate=976 Col=7 Row=M,
                         Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
                                                                                                                                                                                             GSS
                                                                                                                                                                              human
                                                                                                                                                                                                         AQ590563.1 GI:5022215
                                                                                                                                                                                                                            AQ590563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
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          Natl. Acad. Sci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jwallace@u.washington.edu
ce Tagged Connector
3107 row: E column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: sperm; Vector: pBeloBAC11; BAC
E-Coli DH10B"
69 c 71 g 128 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3107 Col=9
/clone=lib="CIT Approved
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57.4%;
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                                                                   e,J.C., Smith,K., Swartzell,S., Furlong,J., Young,J., Zhao,S.,
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Pred. No. 0.0029;
0; Mismatches 80;
          U. S. A.
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     96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102;
Other_GSSs: nc. Contact: Shaying Zhao Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research Part Dr., Rockville,
                                                                             Unpublished (1999)
Other_GSSs: RPCI-24-154D22.TJ
                                                                                                  Tsegaye, G., Geer, K., Krol, M., Shatsman, S., Akinret, B., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                  AZ739176 787 bp DI
RPCI-24-154D22.TV RPCI-24
                                                                                                                                                                                                                                                                                                                      , DNA sequence. AZ739176
                                                                                                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 787)
                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                   AZ739176.1
                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 976 row: M column: 7 Seg primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: Jwallaceeu.washington.edu
Clones are derived from the human BAC library RPCI-11. For I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC,
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Location/Qualifiers
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98 c 117 g 199 t 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=976 Col=7 Row=M"
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/sex="male"
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Pred. No. 0.
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74 Mus >
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACCGGCAGCTGACATGATTGTGGCCTCTCTTGCTTCCTCCCGGTTCTGCTTGCATGGG
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                                                                                                                                                                                                                                                                                                                                                                 AGGATTTCCCAGTTAGTTCC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org), Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC (
page: http://www.tlgr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 154 row: D column: 22
Seq primer: T7
Seq primer: T7
Class: BAC ends.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                             GSS.
                                                                                                                                                                     fly), genomic survey sequence. AL078382
                                                                                                                                                                                                             Drosophila melanogaster genome survey sequence T7 end of BAC: BACR23C23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                          CNSOOKY5
                                                                                                                                                 AL078382.1
                                                                                                         fruit fly.
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="rpci-24-154D22"
/clone_lib="rPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site BamH1; Site BamH1; Sites using MboI partially digested male C57BL/NNA."
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                                                                                              TITLE
JOURNAL
                                                                    MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgattgttatcttcttcatagaattcatcatgtgttctgcgaattgtgcaattctcttat 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATANAANTTAATTTTATATAAGYTTAACCAAATTAGTAAGCAACAGCAATTK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster genome using these BACS. For further information please see http://www.fruitfly.org The BBGP Drosophila please see http://www.fruitfly.org The BBGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2: cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-1999) Genoscope - Centre National BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@ge - Web : www.genoscope.cns.fr)
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                                                                                    Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., E., Worleigh, M., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N52978 399 bp mRNA
yv30b01.s1 Soares fetal liver s
IMAGE:244201 3', mRNA sequence.
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                          N52978.1
                                                Contact: Wilson RK
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/db_xref-"taxon:7227"
/clone_ib-"RPCI-98"
/clone-"BACR23C23"
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Pred. No. 1
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     Box 8501, St. Louis, MO 63108
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                  Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorg Russell,D., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
Other.GSSS: RPCI-24-318G7.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                              ATTGGACTGGTAAACTGCATTGAGTGGGCCAAGAGTTGGAAGGTCTCATCAGCTGATTTC
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1. (bases 1 to 652)
                                                                                                                                                              Mus musculus
                                                                                                                                                                                                    BH045040.1 GI:14828927
                                                                                                                                                                                                                           DNA sequence.
BH045040
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RPCI-24-318G7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="20 week-post conception fetus"
//dev_stage="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
st strand cDNA was primed with a Pac I; oligo(dT) primer
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
30 a 80 c 70 g 117 t 2 others
                                                                                                                                                                                                                                         652 bp DI
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/clone="IMAGE:244201"
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/db_xref="GDB:3793447"
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52.5%;
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Pred. No. 2
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Gebregeorgis,E.,
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
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217 C-TGCTTATGTAGGAAATATGTCTTATAGTTTGACAGATTTAACACA 262
                         458 catacttectaaggaaattttteteecaaaatgeeacaatteaaaaa
                                                          157 CACTGATTTTCTTGACTTTACACATTTTATCTTTAGGGATATATGATCAGTTCTCAATTG 216
                                                                                         398 ctctgctatatgtatctatgatttgtgttttccatagcaaatatgcagggtttatggtcc 457
                                                                                                                                                                                                                 278 tttggcttgccacatggctcggcgttttctattgtgccaaggttgccagcgtcagcc 337
                                                                                                                                                                                             338
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                                                                                                                                                   | cactcttcatctggttgaagatgaggatatccaagctggtcccatggatgatcctggggt 397
                                                                                                                             CTTTTTTTCTTTATCTAAAGTGGAGAGTTAAAAAAGTGATTTTAATAATAATCCTGGCAT 156
                                                                                                                                                                                            TCTGGCTTACTACATGCCTCGGTGTCTTTTTTTTTTTCTCAAGATAGCCAATTTTTTCTAACT 96
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org//acpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                             171
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute for Genomic Research 2 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Spleen/Brain"
/cetl_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="RPCI-24-318G7"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
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Search completed: December 11, Job time: 12533 sec 2001, 02:13:01

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